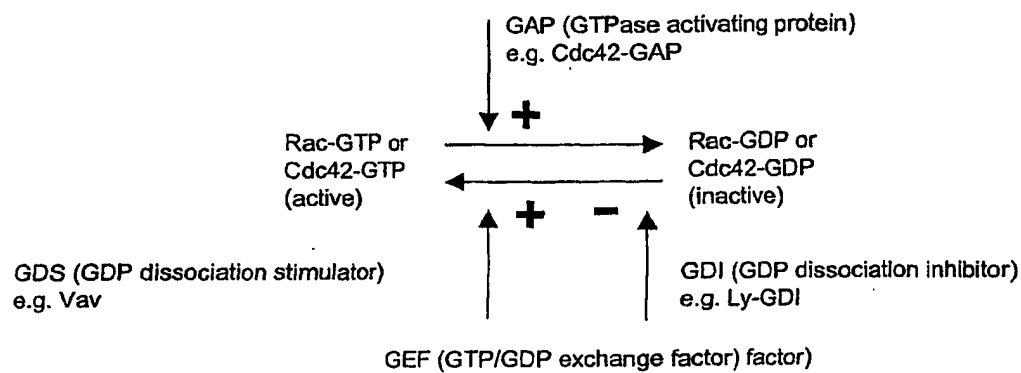


TITLE: GENES INVOLVED IN IMMUNE RELATED RESPONSES
OBSERVED WITH ASTHMA

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Figure 1.

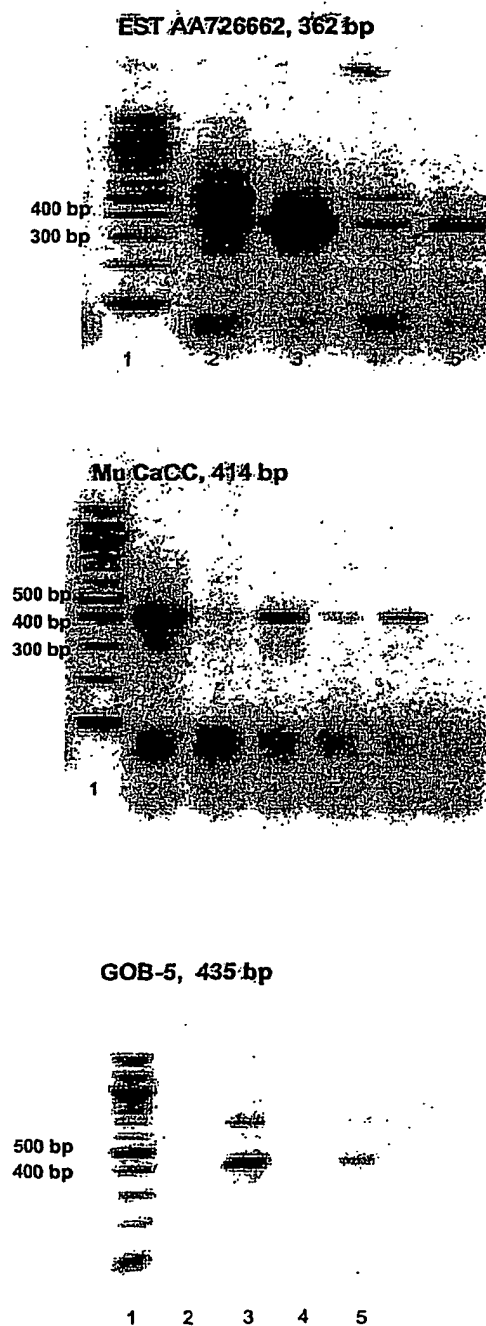


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Figure 2:



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Figure 3.
IgE receptor.

CLUSTAL W (1.81) multiple sequence alignment

```
ige_r_beta_mouse  MDTENRSRADLALPNPQESSAPDIELLEASP-----AKAAPPKQTWRTPLKKEL 50
ige_r_beta_human  MDTESNRRANLALP--QEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQ 58
lr8_mouse         MVQSTVTVNGVKVASTHPQSAHISIHQKSALEQLLG---AVGSLKKFLSWP-----Q 51
lr8_human         MTQNTVIIVNGVAMASRHAQPTHVNVHIHQESALTQLLK---AGGSLKKFLFHPGDTVSS 57
                  *  ..  .: .:  :  .:  .: .:  * .  :

ige_r_beta_mouse  EFLGATQILVGLICLCFGTIVCSVLYVSDPDEEVILLYKLGYPFWGAVLFVLSGFLSIIS 110
ige_r_beta_human  EFLGVTQILTAMICLCFGTVVCSVLQISHIEGDIFFSFRAGYPPWGAIFFSISGMLSIIS 118
lr8_mouse         ARVHYGQLSLGVTQILLGLVSC-ALGVCLYFGPWTELCAFGCAFWSGSAVILAGVGTIVH 110
lr8_human         ARIGYEQLALGVTQILLGVVSC-VLGVCLSLGPWTVLRASGCAFWAGSVVIAAGAGAIHV 116
                  :  *:  .:  :*:  *  *  .  *  .**..  :*  :*:

ige_r_beta_mouse  ERKNTLYLVRGSLGANIVSSIAAGTGIAMLIIN-----LT 145
ige_r_beta_human  ERRNATYLVRGSLGANTASSIAGGTGITILIIN-----LK 153
lr8_mouse         EKROGK-LSGQVSCLLLLACIATAAAATVLGVNSLIRQTSVPYYVEIFS-TCNPLQSSMD 168
lr8_human         EKHPGK-LAGYISSLLTLAGFATAMAAVVLGVNSPINQTBPFYIDTVCDRSDPVFP--T 173
                  *::  *  .  :*  .  .:  *  :

ige_r_beta_mouse  NNFAYMN--NCKNVTEDDGCFFVASFTTELVLMLFLTILAFCSAVLFTIYRIGQELESKK 203
ige_r_beta_human  KSLAYIHHSQCQKFFETK-CFMASFSTEIVVMMLFLTILGLGSAVSLTICGAGEELKGNK 212
lr8_mouse         PGYGTVRYSDSDWKTERCREYLNMMNLFALFCIMLTIVVCILEIVVSVASLGSLRSMY 228
lr8_human         TGYRWMRRSQENQWQKEECRAYMQMLRKLFTAIRALFLAVCVLEKIVVSLVSLGVGLRNL 233
                  .  .:  .  .  .  .:  .:  :  :  :  :  :  :  *  *..

ige_r_beta_mouse  VPDDRLYEELNVYSPIYSELEDKGETSSPVDS----- 235
ige_r_beta_human  VPEDRVYEELNIYSATYSELEDPGEMSPPIDL----- 244
lr8_mouse         GRSSQALNEEESERKLLDGHAPASPAPAKISAIL-- 263
lr8_human         GQSSQPLNEEGSEKRLLGENSEVPPSPSREQTSTAIVL 270
                  .:  :*
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Figure 4

Sequence R1-OS-B1-E5:

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Sequence OtS2-C5:

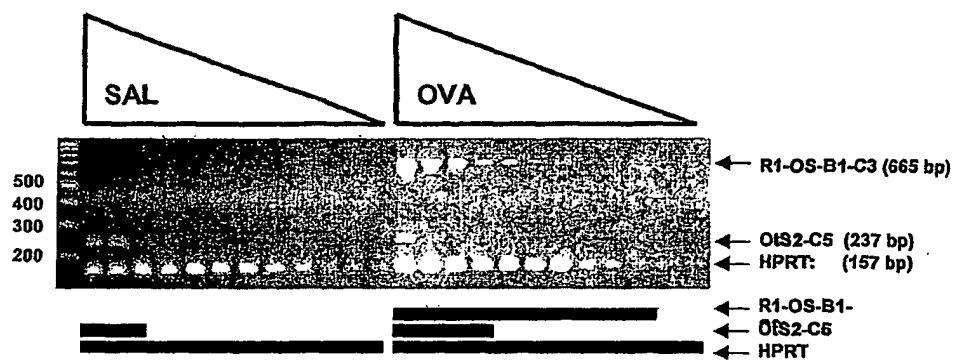
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ncctctnnangggccca

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Figure 5A

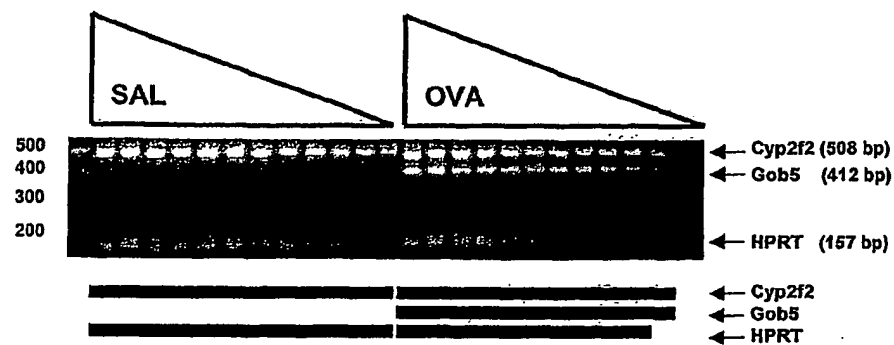


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Figure 5B

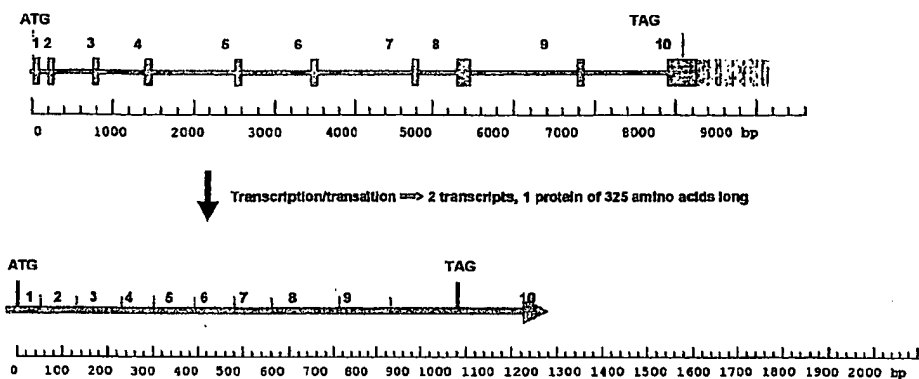


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Figure 6

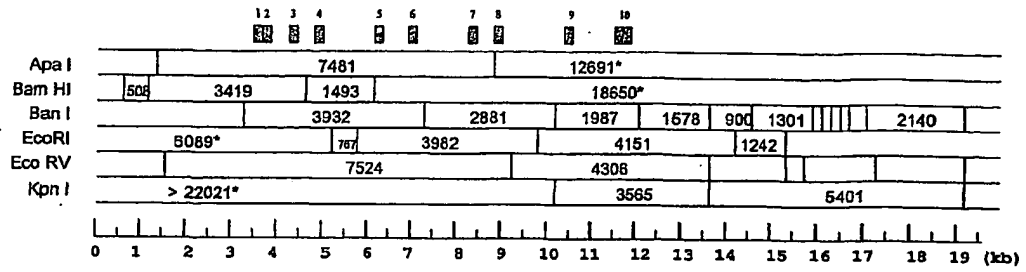


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Figure 7



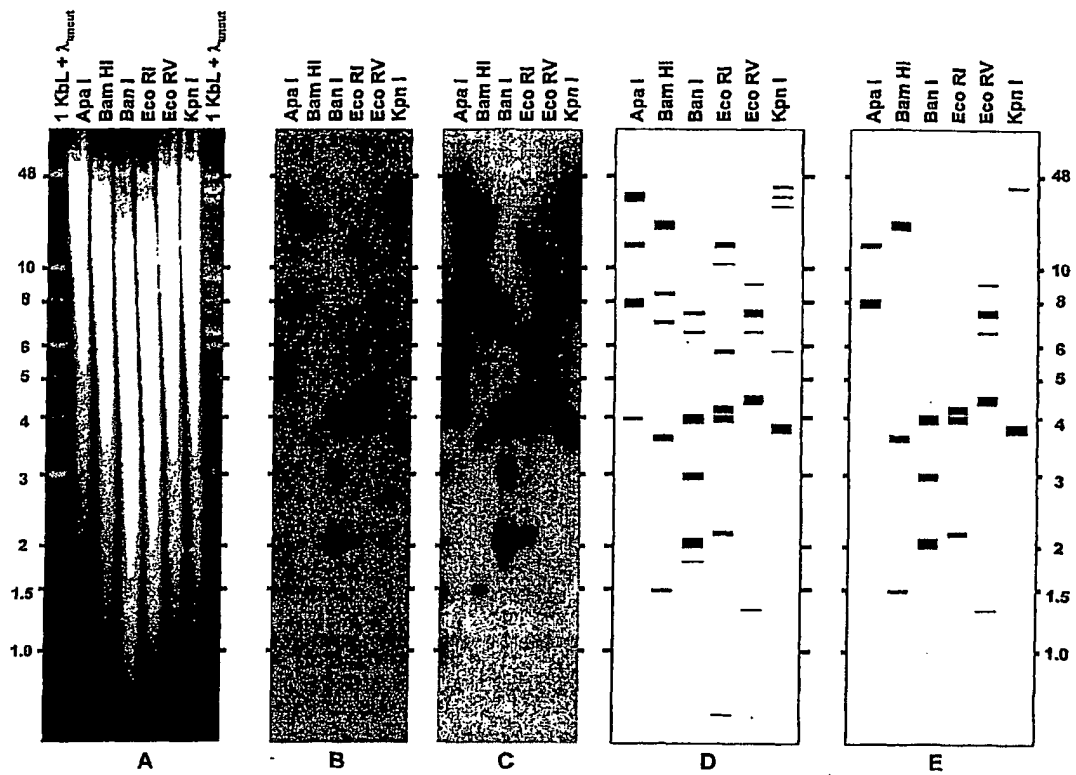
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Figure 8



Filter 180101A 2p127 Hybridisation 24/01/01 2p137 Probe: OtS1-B7-cDNA 47-51 = 1101 bp cDNA (+1: ATG; +978: TAG)
A: EtBr; B, C: 2 and 5 day exposures; D: interpretation (predicted bands red); E: idem, only predicted bands

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Figure 9

BASE COUNT 6308 a 4234 c 4316 g 4761 t
ORIGIN

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Figure 9, Contd.

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9301 gccatctcct cttggagaga taaaagtctt ggtgtgcctg ctaattaaat agcacagcag
9361 acaaagtgtc tgctctaaag cctcacaccc tgagttcaat tcttaggacc ccctgggtaa
9421 taggagagaa tcaactctt aagatgccct ctgacagaca tacctgcact gtggcatatg
9481 cccatccaga catagaagta gacataatta taagaaaaaa tgaagtctct acatgggtct
9541 gcttcacaag cttgaagacc ttgagttaa atccaaagat aaaggaggaat ggggtgagat
9601 ggctcagtag atgaaggcgc ttgctgccaa gcctgacaat ttatcctctg aacctacatg
9661 gttcagagaa ccaacccta taaattgtcc tttagacctc atgtacaggc atattaatat
9721 ccataagaca tatacataga taagcatgca tacaagcata acctgatag atattgaatt
9781 ctctgtgtgt aaatatctc accatgacag cttcaagttt ataatggat gccactgaag
9841 aactgaaaag aaagggtatg tttcttaggt aacctgaat tagcatcatt tgcctctatc
9901 acattaaagc cagccatgag gaaattctat agactcattc tatagactca gaattcttaa
9961 gagccatcca gcaacattag cagaattggg gagggatgaa cagctgtgta attcgtgtgt

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Figure 9, Contd.

10021	gtgcgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt
10081	ttcagacagg	gtctcaactct	agttctatct	ggcctggaac	tcacagaaat	cctgtgggtt
10141	tctgagatta	aaggcatgta	cgtcatgtc	catgcagcta	ggtaccaccc	tatgccaaagt
10201	gaatgtactg	ccataggcta	cagatgtaaa	aatagctgac	accatctaag	cacacatgag
10261	tactcatggc	ctgatatagc	ataaggggaa	aagataatgt	tgtaaagtaga	agtttctgcc
10321	tgaggttggg	gagacaagct	gaaagtagga	aactctcccc	tgactgtcct	cctctttacc
10381	tccagacctt	cctgcagcag	acttctaagg	ctaaaggacc	aacctggatg	ggcctgtcag
10441	acctgaagaa	ggaggccacg	tggctctggg	tagatgggtc	tactctgtca	tccaggtaga
10501	tccagtgaac	aaccagtagt	gtagtccaga	caggctctctg	atgttctgat	agctacctgt
10561	gagtcctatc	ctctctctcc	tcacctctta	gaaataagag	ccacccatat	tagctgatgg
10621	aaggaagttt	tcctaccat	gcacagatag	aatatcagca	aatcccacca	tcaaagcaac
10681	aagaaaaact	tccccctgag	gggtgttaat	tttaatgtag	gctattagta	gaaaatacaa
10741	aataaagtaa	ggccacaggg	taaggggact	attaacattg	aaagatatat	tattgggttg
10801	gggatataaa	tatgttcatt	aagtagcata	aggtttgatc	ccccattgc	atagtctgat
10861	atgggtgtcc	atgcctataa	caccagcagt	tggaggtag	agggagaaga	atcagttcaa
10921	tgttatcttc	agctacaaaa	tgggttctga	gacagcctga	gctacacagg	aagggaaggg
10981	gagagagaaa	gagaaaagca	ggtagggaag	gaaatgtaaa	gaaggggaag	aggacaacag
11041	tagcttaaa	ggagtttata	tggatgttca	ccgatcccac	agcacaacac	agagaacatg
11101	gggaagaacc	acaacaatc	agaataaaaa	ggaaggacac	actgtgggaa	agaaccttta
11161	ctttgttgtc	catgctaag	aacaggagag	actggcttgg	catctattag	tttaccatct
11221	taactttctg	atccctaatt	gtcttacaca	tgcttggcat	gtggcagatg	tattgtggac
11281	cagaatgcaa	gaacccagta	aggaaggcaa	aatccagatt	gattgtttaa	caccacaaaa
11341	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa
11401	atagaaaaac	ccacaccact	ccttcaatgt	aggatataac	aagagtcatt	ttccaaagcc
11461	agcagaccca	ggcatgcccc	catctccaga	ggaaggccca	tctacaatat	gcattctgga
11521	aggaggtaaa	gacattgagt	ttcagaaaag	taaaaaatat	gcattgttca	cagcatgcca
11581	ctggagcaga	ctaactgttt	tctggctgac	tttccagatt	ccagaaatat	tggaaatagag
11641	gggagcctaa	caacatcggt	gaggaagact	gtgtcgaatt	tgctggggat	ggctggaatg
11701	actctaaatg	tgaactcaaa	aagttctgga	tctgcaagaa	gtctgcaacc	ccatgcatg
11761	aaggctagct	catctcctg	cctaccttca	tgccattctg	ccaggcacat	ggatgtgct
11821	cactttctgt	ccagctcctt	cttctctgct	gttggcctca	ggatcgtgaa	aaaggctctg
11881	ggattctctt	ttttatcaga	tttttcatcc	tctgcattta	tcattagttt	atttctgttg
11941	atgtgataaa	actctctaac	caaaaacaac	taaggcagaa	aggggtttat	tttaccttac
12001	attccagatg	agagcagggg	ggtcaggatg	gcaggaaact	aagacaattg	gtcacatcac
12061	atcaaacagc	aggagagag	agaagtatgt	gcaagctaac	gcacacattt	gcttattctc
12121	agttccattt	tcctattcct	atagtttagg	acctctgect	aggaaatggg	gccattcata
12181	gttggctaga	tgttcccacc	tctgttaact	tcaataagac	aagcccccac	agacatgctc
12241	actggccaac	ccaatgcagg	caatacacca	ttgagcctct	tcccagggtga	ctatacgtg
12301	tgtcaggctg	actatcacaa	agggactcac	tattgtcctt	ttgttttcag	gtttctctgg
12361	gcttagggct	cactgttgct	ccccacttcc	agtgcagtta	cctgatgtag	gatgctttca
12421	gaatctgggt	gttttccatt	aacctactcc	atcttccctg	ctgagacaca	tacactcaaa
12481	ggtcagaaga	agacattggg	gttctctttg	atagctcttt	actcccttga	gacaggagtt
12541	ggagttcatt	atttttttag	caaggctggg	gatctgaaag	atccaacatt	tttctgtctc
12601	cactcacctc	ctaaatgaag	ttacagtcac	atgtggccat	gtctggcctc	taacaattac
12661	tagggcttca	aggtcaggcc	ctctttcttg	cacatcagca	ctcttatcca	ctaagcatct
12721	ccccagccat	ttgtctattg	tcaggtagtc	tagtttactg	ttgtgttaat	aaagtcctga
12781	caaaatgcaa	gttggaagag	aaatggatta	tttgacttac	aattctagat	tgtagctcat
12841	ccctgcagga	atatcaagga	aggaaactga	atcagctcat	gatattacat	ccaaaagcag
12901	agagaataag	ttgcatgcat	gcctaatttt	tctaactgaa	tacagtcgcc	caactccaga
12961	gaatgggtgt	gccatattag	gatgggtttc	tgttcaattg	acttaagaca	atgaccccc
13021	ccatggatat	ttctgcaacc	tcgccccaaa	tagaccttat	tgaggatat	tcttctaggt
13081	tgtgtcaaac	tggcaactaa	agctaaccat	cacatcaagt	cctatctgcc	tagtccccct
13141	agacttgatc	ctatctctgt	atactttcat	tctatctgtt	cacttacatc	aacctgctg
13201	aaaacttttg	gctaggaacc	ttccctggcc	tctgtagctc	atcatgcaaa	ctaagcatg
13261	aagatcatcc	ttcttctcca	tctatgactt	ccaggcatca	tcacacaaat	atttcagctc
13321	aggtgctgga	gaaacggctc	agcagtttaag	aatgcactca	ttgctctcct	agaggagcat
13381	agctctcagc	aatcgtacct	gatgaaactc	cagctccagg	gaatctatca	cctttttatg

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Figure 9, Contd.

13441	gcttctgtgt	gcatttgaac	ttatgtgggg	tataaacaca	catcacaca	cattgtacat
13501	gttatatata	tatattatat	atcacatat	acatacacac	atatgtatat	gtataatcag
13561	ctggttccta	tcttggagat	atcatggtgg	atactgagag	ctccaagatt	tctoctcaga
13621	agagaatgtc	ttttccttct	attagacagt	attctattct	attccaattg	atctgtgggg
13681	tgtgtgtgt	gtgtgtgtgt	gtttgtgtgt	gtgcacgcgc	gcgtgcatgc	gcagtcacat
13741	acacaggtac	cacgatttat	tttttattac	tatggctggg	gcagaagtca	ctgagaccct
13801	tctttaagat	ccctatttagc	aaactccata	atthtcccag	aaactatcca	taaagttggg
13861	tttccagcat	ctgacacaa	ctgttcaggc	ctttggctgt	gactgtttgt	ggctttgggt
13921	gtggctgtgg	ccgtggctgc	attcaactgaa	atatctatga	ccagtcctct	aagattgttg
13981	aaagccatat	ttagaatgta	gcttgtcaat	atgaccattt	atgaaaacag	cagtactaag
14041	tttctctccag	gtgtatggcc	tcaccagctg	tggatttttg	gtcaaattht	gtaccagtca
14101	tgaattcctt	cctaaagaga	aggcatcaat	acagtaagaa	atagttggac	actcccataa
14161	cagtcatgca	tcagtggaaa	catatttaat	aaagaaaata	caacacacaa	ccactthtcc
14221	aaacaacttt	tgctttattt	gtttttttta	aaagaaagcc	aatatttact	tttcatcttt
14281	agtcttaata	ttaattttta	aaagatgtgt	gtgaatacct	ttttgcacat	tcctttccta
14341	atgcctttta	tctcagctga	acatctcaac	ttcttgtcgt	tgtctcttca	tcttaacatc
14401	tgtatttcca	ctctctctct	gacttaatat	ctgggtccac	aaactccact	aaaaattctg
14461	tctctactgg	aggccacatt	ggtactagga	actccaaaag	tctcctgatc	taccaaagac
14521	cacactggca	ttaggaaaca	aacaaacaaa	caaaacaaaca	aacaaaacaa	aacttcagtt
14581	acctggaacc	tcagagggca	tgccagttcc	cagaacccca	gaatttcaga	ggttagtcca
14641	catagggcac	caaaccactg	atggagacac	actactagac	ctgaagactt	attgggtcatc
14701	agaaccatag	gttactcaaa	ccagaagacc	agaaaggaaa	ccaaagcagt	gggaaaaaac
14761	atccaacaaa	gataaagtca	gcaatgatca	cctaaacata	taataaccaa	accagatga
14821	ctagaggcca	gcatatgaac	acagtcaaca	atatccaagg	caatacatca	ccaccagagc
14881	tatctctcta	cagaaagcac	tgaatttttt	taacacagct	gaagcacatg	aaaattacct
14941	taaatccaat	cttatgaaga	taatagagac	ctthtaagaa	gaaatacaaa	aaaaaaaaac
15001	cttaaacaaa	tcaggggtgag	agtaagggag	gcaaacagat	aaaggaatgt	gtttaagatg
15061	tgaaaataga	aatagacgaa	taaatgaaat	acaaactgat	ggaatactgg	aatggaaaaa
15121	tctaggtatg	ttaacagaa	ctacagacag	aagtatcact	aacagaatac	aagagatgga
15181	aaaggatata	aggcatagaa	gataagatag	aagaaactaa	tatggcattt	aaaaatgtt
15241	atatctaaaa	aggctcctgac	acaaaatgtt	caggaaatca	aggaaactat	aaagagacca
15301	aacctaagaa	caataggaat	agaagaggga	gatttccagc	tcagaattct	taggaaaaaa
15361	tacctaacct	aaagaagggtg	atgcctataa	aggtacaaga	aacatacaga	agaccataata
15421	tgttggacca	gaaaagaaaag	tcttcccacag	agataataat	caaaacacta	aatgtacaga
15481	gggaagaata	ttaaaagcta	aaagaggaaa	aggcacaaaa	aaaaccaaca	acaacaacaa
15541	aaacatgtaa	aggcaaacct	agtagaatta	tgccctactt	ctcaacagaa	aatctaaaaa
15601	gctagaaaag	catggacaga	tgtattacaa	actctgagag	accacagata	tcagcccaga
15661	cgactgtaac	aagcaaaaact	ttcaatcacc	atagatggag	aaaacaagat	attctatgtc
15721	aaacccaaat	ctaaatacga	tctttctatt	aatccagccc	tacagagggt	acaagaaggga
15781	aaacttctgt	ggtccgggac	ccgcccgaact	taggaaattt	gtctgaacag	gtgagagggt
15841	gcgccagaga	acctgacagc	ttctggaaaca	ggcagaagca	cagaggcgct	gaggcagcac
15901	cctgtgtggg	ccggggacag	ccggccacct	tccggaccgg	aggacagggt	ccacccggc
15961	aggggaggcg	gcctaagcca	cagcagcagc	ggtcgccatc	ttggtccggg	accgcccgaa
16021	cttaggaaat	tagtctgaac	aggtgagagg	gtgcgccaga	gaacctgaca	gcttctggaa
16081	caggcagaag	cacagaggcg	ctgaggcagc	accctgtgtg	ggccggggac	agccggccac
16141	cttccggacc	ggaggacagg	tgcccaccgg	gcaggggagg	cggcctaagc	caacagagca
16201	gcggctcgcca	tcttgggtccg	ggaccgcggc	aacttaggaa	attagtctga	acagggtgaga
16261	gggtgcgcca	gagaacctga	cagcttctgg	aacaggcgga	agcacagagg	cgctgaggca
16321	gcacctgtg	tgggcccggg	acagcggg	accttccgga	ccagaggaca	ggtgcccacc
16381	cggctgggga	ggcgccctaa	gccacagcag	cagcgggtgc	catcttgggt	cgggaccggc
16441	cgaacttagg	aaattagtct	gaacagggtga	gagggtgcac	cagagaacct	gacagcttct
16501	ggaacaggca	gaagcacaga	ggcgctgagg	cagcaccctg	tgtgggctgg	ggacagccgg
16561	ccaccttccg	gaccagaggga	caggtgcccg	cccggtggg	gaggcgacct	aagccacagc
16621	agcagcggtc	gccatcttgg	tccgggaccc	gccgaactta	gggaattagt	ctgaacaggt
16681	gagagggtgc	gccagagaac	ctgacagctt	ctggaacagg	cgggaagcaca	gagggcgctga
16741	ggcagcacc	tttggggcc	ggggaacccc	agccaccgtc	cggaccggag	gacaggtgcc
16801	tgtccggctg	gggaggcggc	ctaagccaca	gcagcagcg	tgcctatctt	ggtccgagac

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Figure 9, Contd.

16861	ccgccgaact	taggaaatta	gtctgaacag	gtgagagggg	gcgccagaga	acctgacagc
16921	ttctggaaca	ggcagaagca	cagaggcgct	gaggcagcac	cctgtgtggg	ccggggacag
16981	ccggccacct	tccggaccgg	aggacagggt	cccacccggc	aggggaggcg	gcctaagcca
17041	cagcagcagc	ggtcaccatc	ttgggtcccg	gactccaagg	aacttaggaa	tttagtctgc
17101	ttagggtgaga	gtctgtacca	cctgggaact	gccaaagcaa	cacagtgtct	gagaaaggctc
17161	ctggtttggg	ccttcttctt	cggccaggag	gaggtccaaa	tacaagatat	ctgcgcacct
17221	tccctgt aag	agagcttgcc	agcagagagt	gctctgagca	ctgaaaactca	gaggagagaa
17281	tctgtctccc	aggtctgctg	atagacggta	acagaatcac	cagaagaaca	atctcta aac
17341	agagtcaact	ataactacta	actccagaga	ttaccagatg	gcgaaaggta	aacggaggaa
17401	tcttactaac	aggaaccaag	accactcacc	atcaccagaa	cccagcacac	ccacttcgcc
17461	cagtccaggg	aaccccaaca	cacctgagaa	cctagaccta	gatttaaaag	catatctcat
17521	gatgatggta	gaggacatca	agaaggactt	taataaatca	cttaagaaa	tacaggagaa
17581	cactgctaaa	gagttacaag	tctttaaaga	aaaa caggaa	aacacaatca	aacaggtaga
17641	agtccttaca	gaaaaagagg	aaaaaacata	caaacagggtg	atggaaaaatg	aacaaaacca
17701	tactagacct	aaaaagggaa	gtagacacaa	taaa gaaaac	tcaaagcgag	gc aacgctag
17761	agataga aac	cctaggaaag	aaatctggaa	ccatagattt	gagcatcagc	aa cagaatac
17821	aagagatgga	agagagaatc	tcaggtgcag	aagattccat	agagaacatc	ggcacaacaa
17881	tcaaagaaaa	tggaaaatgc	aaaaagatcc	taactcaaaa	tatacaggaa	atccaggaca
17941	caataagaag	accaaa cgta	cggataatag	gagtg gatga	gaatgaagat	tttcaactca
18001	aagggtccagc	aaacatcttc	aacaaaatta	ttgaagaaaa	cttcccaaat	ctaaagaatg
18061	agatgcatat	gaacatacaa	gaagcctaca	gaactccaaa	tagactggac	cagaaaagaa
18121	attcctcccg	acacataata	atcagaacat	caaatgcact	aaataaagat	agaatactaa
18181	aagcagt aag	ggaaaaagggt	caagtaacat	ataaaggcaa	gcctatcaga	at tacaccag
18241	at ttttcacc	agagactatg	aaagccagaa	gagcctggac	agatgttata	cagacactaa
18301	gagaacacaa	actgcagccc	aggctactat	acccagccaa	actctcaatt	atcatagagg
18361	gaga aaccaa	agtattccac	gacaaaacca	aattcacgca	ttatctctcc	acgaatccag
18421	cccttca aag	gataataaca	gaaaaaaaacc	aatacaagaa	cgggaacaac	gccctagaaa
18481	aaacaagaag	gtaatccttc	aacaaaaccta	aaagaagaca	gccacaagaa	cagaatgccca
18541	cctttaacaa	ctaaaataac	aggaagcaac	aattactttt	ccttaatatc	tcttaacatc
18601	aatgggtctca	actcgccaat	aaaaagacat	agactaacaa	ctggctacac	aaacaagacc
18661	caacattttg	ctgcttacag	gaaactcatc	tcagagaaaa	agatagacac	ta cctcagaa
18721	tgaagggtctg	gaaacaattt	tccaagcaaa	tggtatgaag	aaacaagcag	gagtagccat
18781	cctaataatct	gataagatga	cttccaaccc	aaagtcatca	aaaaagacaa	ggagggcac
18841	ttcatttctca	tcaaaggtaa	aatcctccaa	gaggaactct	caattctgaa	tatctatgct
18901	ccaatacaaa	gagcagccac	attcactaaa	gaaactttag	taaagctcaa	agcacacatt
18961	gcgcctcaca	caataatagt	gggagacttc	aacacaccac	tttcaccaat	ggacagatca
19021	tggaaacaga	aactaaacag	ggacacactg	aaactaacag	aagtgtgaa	acaaatggat
19081	ctgacagata	tctacagaac	at tttaccct	aaaa caaaag	gatatacctt	cttctcagca
19141	cctcatggta	ccttctccaa	aattgaccac	ataataggtc	acaaatcagg	cctcaacaga
19201	ttcaaaaata	ttgaaattgt	cccatgtatc	ctatcagatc	accatgcact	aaggctgac
19261	ttcaataaca	aaataaataa	cagaaagcca	acattcacat	ggaaactgaa	caacactctt
19321	ctcaatgata	ccttggtcaa	ggaagggaata	aaga aagaaa	ttaaagactt	tttagagttt
19381	aatgaaaatg	aagccacaac	gtacccaaac	ctttgggaca	caatgaaagc	at tttctaaga
19441	gggaaactca	tagctatgag	tgcttcaag	aaaaaacggg	agagagcaca	tactagcagc
19501	ttgacacaca	tctaaaagct	ctagaaaaaa	aggaagcaat	tcacccagag	gagtagacgg
19561	caggatataa	tcaaactcgg	ggtgaaatca	accaagtga	cagagactat	tcagataacc

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Figure 10

1	MSDSTEAKMQ	PLSSMDDDEL	MVSGSRYSIK	SSRLRPNSGI	KCLAGCSGHS	QVPLVLQLLS	60
61	FLFLAGLLLI	ILFQVSKTPN	TERQKEQEKI	LQELTQLTDE	LTSRIPISQG	KNESMQAKIT	120
121	EQLMQLKTEL	LSRIPIFQGQ	NESIQEKISE	QLMQLKAELL	SKISSFVKD	DSKQEKIYQQ	180
181	LVQMKTLEFR	LCRLCPWDWT	FLLGNCYFFS	KSQRNWDAV	TACKEVKAQL	VIINSDEEQT	240
241	FLQQTSKAKG	PTWMGLSDLK	KEATWLWVDG	STLSSRFQKY	WNRGEPNNIG	EEDCVEFAGD	300
301	GWNSDKCELK	KFWICKKSAT	PCTEG				325

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Figure 11

Sequence format is Pearson

Sequence 1: AAF77072 404 aa

Sequence 2: OtB7-ORF 325 aa

Sequences (1:2) Aligned Score: 45

```

AAF77072      MSDSKEPRLQQQLGLLEEEQLRGLG-----FRQTRGYKSLAGCLGHG--PLVLQLLS 49
OtB7-ORF      MSDSTEAKMQPLSSMDDDELMVSGSRYSIKSSRLRPNSGICKLAGCSGHSQVPLVLQLLS 60
              ****.*.:.* *. :.:.* * : * . * *.***** *. *****

AAF77072      FTLLAG---LLVQVSKVPSSISQEQSRQDAIYQNLTLQKAAVGELSEKSKLQEIYQELT 105
OtB7-ORF      FLFLAGLLLIILFQVSKTPN--TERQKEQEKIQLQELTQLT---DELTSR----- 104
              * :*** :*.*****. :.:.*.: * *:*****. :*.:

AAF77072      QLKAAVGELPEKSKLQEIYQELTRLKAAVGELPEKSKLQEIYQELTWLKAAVGELPEKSK 165
OtB7-ORF      ---IPISQGNESMQAKITEQLMQLKTEL----- 130
              .:.: :.* :* :.* :*.:

AAF77072      MQEIYQELTRLKAAVGELPEKSKQOEIYQELTRLKAAVGELPEKSKQOEIYQELTRLKAA 225
OtB7-ORF      -----LSRIPIFQGN--ESIQEKISEQLMQLKAE--LSKISSFP----- 167
              *:.* :* :* :.* :.* :*.: *.: *.

AAF77072      VGELPEKSKQOEIYQELTQLKAAVERLCHPCPWEWTFQGNCFMSNSQRNWHD SITACK 285
OtB7-ORF      ---VKDDSKQEKIYQQLVQMKTFLRLCRLCPWDWTFLLGNCYFFSKSQRNWDAVTACK 224
              : :.***:***.*.*.: : ***: ***:***: *****:*****:*.:***

AAF77072      EVGAQLVVIKSAAEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNR 345
OtB7-ORF      EVKAQLVIINSDEEQTFLO-QTSKAKGPTWMGLSDLKKEATWLWVDGSTLSSRFQYWNR 283
              ** *****:.* ***.*** *:.: : *****:*.** *****. * . *:****

AAF77072      GEPNNVGEEDECAEFSGNGWNDDKCNLAKFWICKKSAASC SRDEEQFLSPAPATPNPPPA 404
OtB7-ORF      GEPNNIGEEDCVEFAGDGWNDSKCELKKFWICKSATPCTEG----- 325
              *****:*****.*.*:*****.*.* *****:*.:..

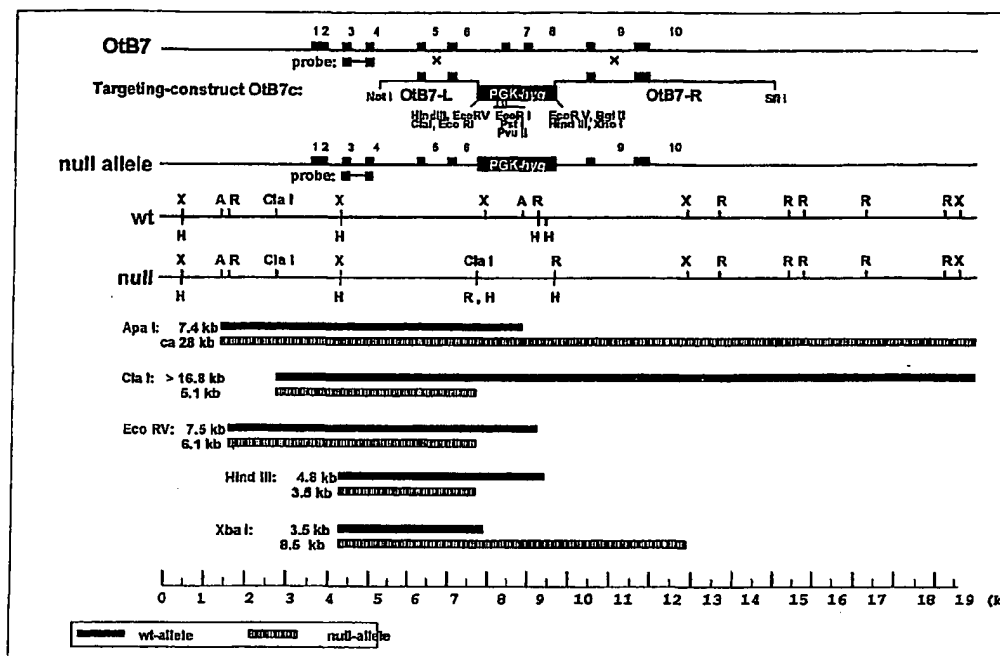
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Figure 12

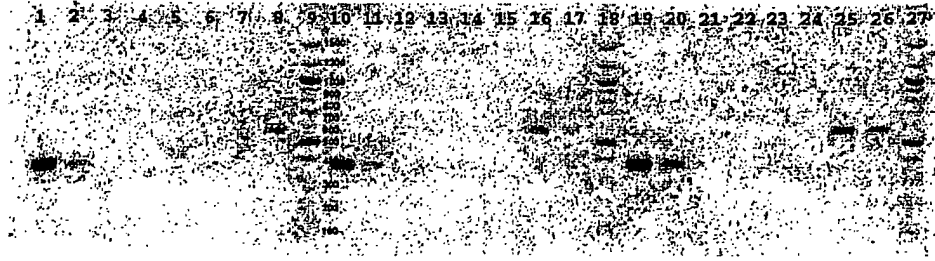


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Figure 13



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FIGURE 14

Gob-5 --MSLSKSPVFLLIHLHLEGALVSESL-----IQNNNGYEGIVIAIDHDPFDEALIQH 52
HuCLCA1 --MGPPFKSSVFLIHLHLEGALSNLSL-----IQNNNGYEGIVVVAIDPNVPDETLLIQ 52
HuCLCA4 --MGLPRGFVFLVLVLCILH-QNSTSF-----IKLNNNGFEDIVIVIDPSPVDEKILIQ 51
MuCaCC --MVPGLQVLLFLTLHLQL-NTSSSM-----VHLNSNGYEGVVIATNPSPVDEKLIPS 51
HuCLCA2 MTQRSIAGPINCILKFVTLVALSSSELPLFAGAGVLQDNGVYGLLIATNPQVFNQNLISN 60
: * : * : *

Gob-5 IKDMVTQASPYLFEATGKRFYFKNVAILIPESWIAKPEYTRPKLETFNADVLVSTTSPL 112
HuCLCA1 IKDMVTQASLYLFEATGKRFYFKNVAILIPETWTKADYVRPKLETYKNADVLVAESTPP 112
HuCLCA4 IEDMVTATSYLFEATGKRFYFKNVAILIPENWKNPQYKRPKHENKHADVIVAPPTLP 111
MuCaCC IKEMVTQASPYLFEASGGRVYFRNISILVPMTWSKPEYLMPPKRESYDKADVIVADPHLQ 111
HuCLCA2 IKEMITBASPYLFNATKRRVFRNRIKILPATWKAN-NNSKIKQESYEKANVITVDWYGA 119
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 GNDEPYTEHIGACSEKGIIRIHLTPDFLAGKCLTQ-YGPQDRTFVHEWAHFRWGVFNEYNN 171
HuCLCA1 GNDEPYTEQMGACSEKGERIHLTPDFIAGKCLAB-YGPGKAFVHEWAHLRWGVFDEYNN 171
HuCLCA4 GRDEPYTKQFTECEKGEYIHFTPDLLLGKKQNE-YGPPGKLFVHEWAHLRWGVFDEYNE 170
MuCaCC HGDDPYTLQYGCCEDRGQYIHFTPNFLLTDNLRI-YGPRGRVVFHEWAHLRWGVFDEYNN 170
HuCLCA2 HGDDPYTLQYRCCEKGEYIHFTPNFLLTDNLRTAGYGSRGVVFHEWAHLRWGVFDEYNN 179
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 DEKFYLSKGGK-PQAVNCSAAITGKNQVRRQGGSGCTGKCYIDRVTLGLYKDNVCFVDPDP 230
HuCLCA1 DEKFYLSNGR-IQAVNCSAGITGTNVVKKQGGSGCTK-RDPFNKVTGLYEKGCBEFVLQS 229
HuCLCA4 DQPFYRAKSKKIEATCSAGISGRNRVYKQGGSGCLSR-ACRIDSTTKLYGKDCQFFPDK 229
MuCaCC DQPFYNSRNTIEATCSITGTNVVHNCERGNCTR-ACERDSKTRLYEPKCTFIPDK 229
HuCLCA2 DKPFYINGONQIKVTTCSSDITG---IFVCEKGCPCQE-MCIIIS---KLFKEGCTFFYNS 232
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 HQNEKASIMFNQININSVVEFCTEKNHMQEAPNDQNQRCLNRSTWEVIEQSEDFKQTTPM- 289
HuCLCA1 RQTEKASIMFAQHVDISIVEFCTEQNHNEKAPNQKQCNLRSTWEVIRDSEDFKKTTPM- 288
HuCLCA4 VQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNEDFKNTIPM- 289
McACC IQTAGASIMFMQNLNSVVEFCTEQNHNAEAPNLQNMKNRRSTWDVITKSADFPQNAFMR 288
HuCLCA2 TQNTATASIMFMQSLNSVVEFCNASTHNEAPNLQNMCLSRSAWDVITDSADFHSPFPMN 292
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 -TAQPPAPTFSLQIGQIRIVCLVLDKSSGSLNDDRLEWLNQASRLFLLQTVEQGSWVGIV 348
HuCLCA1 -TTQPPNPTFSLQIGQIRIVCLVLDKSSGSLATGNRLWELNQAGQLFLLQTVELQGSWVGIV 347
HuCLCA4 -VTTPPPPVFSLILKIRQIRIVCLVLDKSSGSGGGRDRLWLNQAAHQLFLLQTVELNGSWVGIV 347
McACC GTEAPPPPTFSLKSKRRRVCLVLDKSSGSHDKEDRLTRNNQAAELYLTLQIVEKESMVGLV 349
HuCLCA2 GTELPPPTFSLVQAGDKVVCVLDVSSSKAEADRLLQLQAAAEFLMQVIEHTFVGIA 352
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 TFDSAAYVQSELEKQLNSGADRELLIKHLPTVSAGGT--SICSGLRTAFTVIKKKYP-TDG 405
HuCLCA1 TFDSAAYVQSELIQNSGDRPTLAKRLPAASGGT--SICSGLRSAFTVIREKKYP-TDG 404
HuCLCA4 HFDSTATVKNLIIQIKSSDERNTLMAGLPTYPLGGT--SICSGIKYAFQVIGELHSQLDG 405
McACC TFDSAANKYNYLIKTTSSBDYQKITTANLPQASGGT--SICHGLOAGFQATTSDDQSTSG 407
HuCLCA2 SFDSGEITRAQLQGLNSNDRKLLVSLPTTVSAKTDISIISGLKKGFEVVEKLNGKAYG 412
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 SEIVLLTDGEDNTISSCDFLVQSGAIHTVALGPAAAKELEQLSKMTGGQLQTYASDQVQ 465
HuCLCA1 SEIVLLTDGEDNTISSCFNEVQSGAIHTVALGPSAAQELBELSKMTGGQLQTYASDQVQ 464
HuCLCA4 SEIVLLTDGEDNTIASSCIDEVQSGAIVFIALGRAADEAVIEMSKITGGSFIYVSDAQV 465
McACC SEIVLLTDGEDNGIISCFEAVERSGAIHTIALGPSAARELETSLDMTGGFIFYANKLDN 467
HuCLCA2 SVMLLVTSODDKLLGNCLFTVLSSSGSTIESIALGSSAAPNLEELSLTGGKLFVFPDISN 472
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 NNGLVDAPFAALSSSGNAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVGKDTFLITWTT 525
HuCLCA1 NNGLIDAFGALSSSGNGVQSRSIQLESKGLTLQNSQWMNGTIVDSTVGKDTFLITWTT 524
HuCLCA4 NNGLIDAFGALTSGMTDGSQSKSLQLESKGLTLNNSAWMNDTVIIDSTVGKDTFLITWNS 525
McACC --SLIDAFSRISSTSGSVSQALQLESKFLDVRAGAWINGTVPDSTVGNDTFFVITWNV 525
HuCLCA2 SNKNIDAFSRISSTGDIQFQHIQLESTGENVKPHQLEKNTFTVDNTVGNDTMFLVTWQA 532
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Gob-5 H-PPTFIWDPSGV--EQNGFILDIT-TRVAYLQVPGTAKVGFWKYSIQASS---QTLTL 578
HuCLCA1 Q-PPQILLWDPSGQ--KQGGFVVDKN-TRMAYLQIPGIKAVGTWKYSIQASS---QTLTL 577
HuCLCA4 L-PPSISLWDPSGT--IMENPTVDAT-SKMAYLQISPGTAKVGTWYNLQAKAN-PETLL 580
McACC K-KPRIILLQDPKGGKYTTSDFQDDKLNIRASRLQIPGARTGTWTYSITGTSK---QLITM 582
HuCLCA2 SGPPRIILLFDPDGRKYTNNRIITNL-PRITASLIPGTAKPGHWITTYLNNTHSHIQALKV 591
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

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FIGURE 14, CONTD.

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Gob-5      TVTSRAASATLPPITVTVPVNKNTGKFPSPVTYASIROGASPILRASVTALIESVNGKT 638
HuCLCA1    TVTSRASNATLPPITVTSKNTKDTSKFPSPLVVYANIRQGASPILRASVTALIESVNGKT 637
HuCLCA4    TVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHT 640
McACC      TVTTRARSPTMEPLLATAHMSQSTAQYPSRMIVYARVVSQGFLPVLGANVTALIEAEHG HQ 642
HuCLCA2    TVTSRASNSAVPPATVEAFVERDSLHFPHPVMIYANVKQGFYPILNATVTATVEPETGDP 651
          ***:*** . . . : * . . . : . : * : : ** : * * * * : * . * .


Gob-5      VTLELLDNGAGADATKNDGVYSRFFTAFDANGRYSVKIWALGGVTSRDRQRAAPPKNRAMY 698
HuCLCA1    VTLELLDNGAGADATKDDGVYSRYFTTYDTNGRYSVKVRALGGVNAARRRVIPOQS GALY 697
HuCLCA4    EVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSKVRHGGANTARLKLRPPLNRAAY 700
McACC      VTLELDNGAGADTVKNDGIYTRYFTDYHGNSRYSKLVRVQAQRNKTRLSLR-QKNKSLY 701
HuCLCA2    VTLRLDDGAGADVIKNDGIYSRYFFSFAANGRYSKLVHVNHSFSPSISTPAHSIPGSHAMY 711
          . . . * : * * * * * : * * * * * : . : * : * * * * * : . : *

Gob-5      IDGWIEDGEVRMNP RP PETS--YVQDKQLCFSRTSSGGSEFVATNVPAAPPIPLDFPPCQI 756
HuCLCA1    IPGWIEWDEIQWNP RPPEINKDDVQHKQVCFSRTSSGGSEFVASDVFN-APIPOLFPFGQI 756
HuCLCA4    IPGWVVNGEIEANP RPPEID-EDTQTLEDFSRASGGAFVVSQVPS-LPLPQYPPSQI 758
McACC      IPGYVENGKIVLNP RPDPVQEEAIEATVEDFNRTVSGGSFTVSGAPPDGDHARVFPFSKV 761
HuCLCA2    VPGYTANGNIQMNA PRKSVG-RNEEERKNGFSRVSSGGSFVGLGVA-GPHDPVFPFCKI 769
          : : . . . : * . * . : . : * : * * * * * : . : * : * :

Gob-5      TDLKASIQQQNLVNLWTAPGDDYDHGRASNYIIRMSTSIVDLRDHFNTSLQVNTTGLIP 816
HuCLCA1    TDLNAEIHGGSLINLTWTAPGDDYDHGTAHKYIIRISTSILDLRDKFNESLQVNTTALIP 816
HuCLCA4    TDLDATVHEDKII-LTWTAPGDNFDVGKVRQYIIRISASILDLRDSFDDALQVNTTDLSP 817
McACC      TDLEAEFIG-DYIHLTWTAPGKVLNDRGHRHYIIRMSQHPLDLQEDFNNTLVNAGSLIP 820
HuCLCA2    IDLEAVKVEEELT-LSWTAPGEDFDQGGQATS YEIRMSKSLQNIQDDFNAILVNTSKRNP 828
          . . . * : * * * * * : * * . * * * * : : : : * : : * :

Gob-5      KEASSEEI FEFELGGNTFG-----NGTDIFIAIQAVDKSNLKSEISNIARVS VFI 866
HuCLCA1    KEANSEEVFLFKPENITFE-----NGTDLFIAIQAVDKVDLSEISNIARVS LFI 866
HuCLCA4    KEANSKESFAFKPENISEE-----NATHIFIAIKSIDKSNLTSKVSNI AQVTLFI 867
McACC      KEAGSKETFKFKPETFKIA-----NGIQLYIAIQADNEASITSEVSNIAQAVKLT 870
HuCLCA2    QQAGIREIFTTFSPQISTNGPEHQPNGETHESHRIYVAIRAMDRNSLQSAVSNIAQAPLFI 888
          : * . . * * . . . : . : * * * * : . . * * * * * :

Gob-5      PAQEP---PIPEDSTPPCPDISINS--TIPGIHVLKIMWKWLGEMQVTLGLH----- 913
HuCLCA1    PPQTTPPETPSPDETSAPCPNIHINS--TIPGIHLKIMWKWIGELQLSIA----- 914
HuCLCA4    PQANP-DDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI----- 917
McACC      SLEDS-----ISALGDISAICMTIWLGLTVIFNSILN----- 901
HuCLCA2    PPNSD----PVPARDYLILKGVLTA MGLIGIICLIIVVTHHTLSRKKRADKKENGTKLL 943
          : : * : :
```

 Conserved cysteines
VWLTGGEN von Willebrand factor type A domain

gnl|Smart|smart00327, VWA, von Willebrand factor (vWF) type A domain; VWA domains in extracellular eukaryotic proteins mediate adhesion via metal ion-dependent adhesion sites (MIDAS). Intracellular VWA domains and homologues in prokaryotes have recently been identified. The proposed VWA domains in integrin beta subunits have recently been substantiated using sequence-based methods (Ponting et al. Adv Prot Chem (2000) 54:185-244).

 MIDAS motif

Affinity regulation: MIDAS Bonds in CD11's

The metal ion-dependent adhesion site (MIDAS) is believed to be the site on the alpha chain of LFA-1 (alpha-L, CD11a) which binds ligand (ICAM-1, ICAM-2, or ICAM-3). Although it is likely to be a critical portion of the ligand-binding site, other parts of LFA-1 may also make important contributions, notably the MIDAS site on CD18, and the 4th and 5th repeats of CD11a. The MIDAS motif consists of DxxSxS...T...D, and is equally central to ligand binding for both CD11a/CD18 (LFA-1) and CD11b/CD18 (Complement receptor type 3, CR3).

Forward primer

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FIGURE 15

```
BE655906      AGTCACTGGCGATCTGAAAAGTGTCTAGAGCAGGATCTAGCTGACTCTAAGATTGCAGGG 60
OtS2-D10      -----GATCTAGCTGACTCTAAGATTGCAGGG 27
CD59          AGTCACTGGCGATCTGAAAAGTGTCTAGAGCAGGATCTAGCTGACTCTAAGATTGCAG-- 63
               .....*****

BE655906      TTGAAGGTGTCTGTGAAGCCTGTGGAACTGCTGCTTTAAATCTTCAATCTGGCTGGG 120
OtS2-D10      TTGAAGGTGTCTGTGAAGCCTGTGGAACTGCTGCTTTAAATCTTCAATCTGGCTGGG 87
CD59          -----

BE655906      GATGTGGCTCAAGATAGTGTGCTGATGGTGGCCTGGCTTGGTTCTTCATATATTAATAAT 180
OtS2-D10      GATGTGGCTCAAGATAGTGTGCTGATGGTGGCCTGGCTTGGTTCTTCATATATTAATAAT 147
CD59          -----AT 65
               **

BE655906      TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 240
OtS2-D10      TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 207
CD59          TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 125
               *****

BE655906      TGTGTTCGTGTTCCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 300
OtS2-D10      TGTGTTCGTGTTCCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 267
CD59          TGTGTTCGTGTTCCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 185
               *****

BE655906      TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCGTCTCTATGCTGTAGC 360
OtS2-D10      TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCGTCTCTATGCTGTAGC 327
CD59          TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCGTCTCTATGCTGTAGC 245
               *****

               <-----
               reverse

BE655906      CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATG----- 407
OtS2-D10      CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATGGTGATC----- 378
CD59          CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATGGTGAGATCATTAT 305
               *****
               -----
               primer
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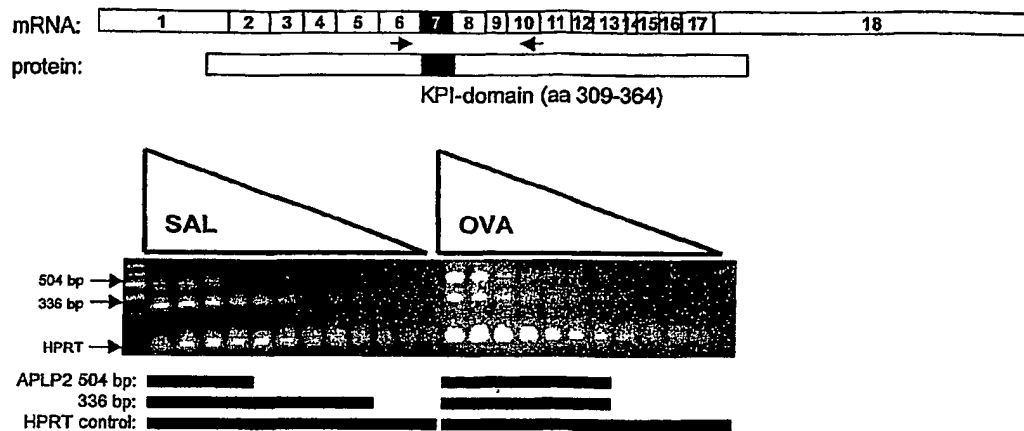
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Figure 16

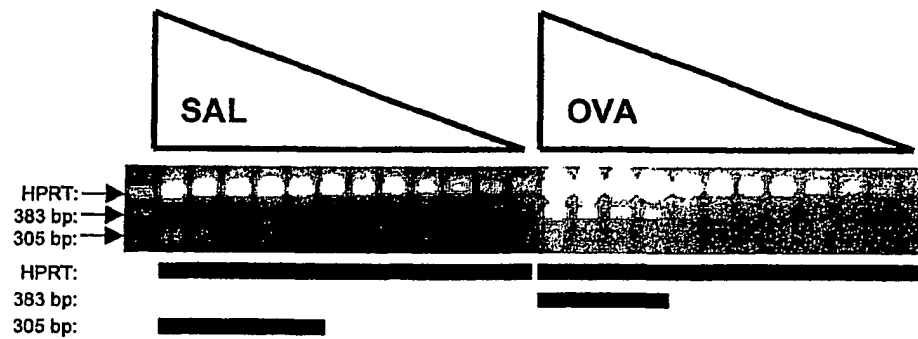


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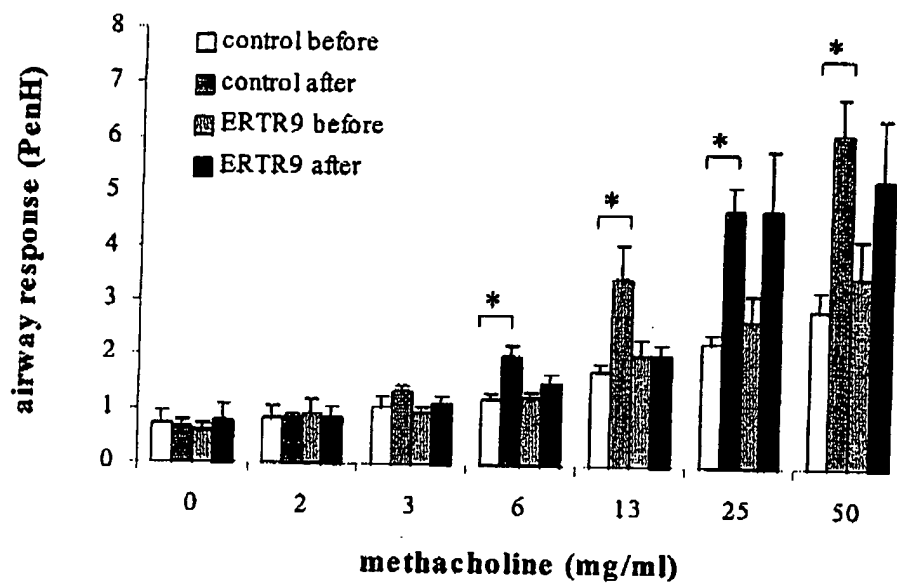
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Figure 17



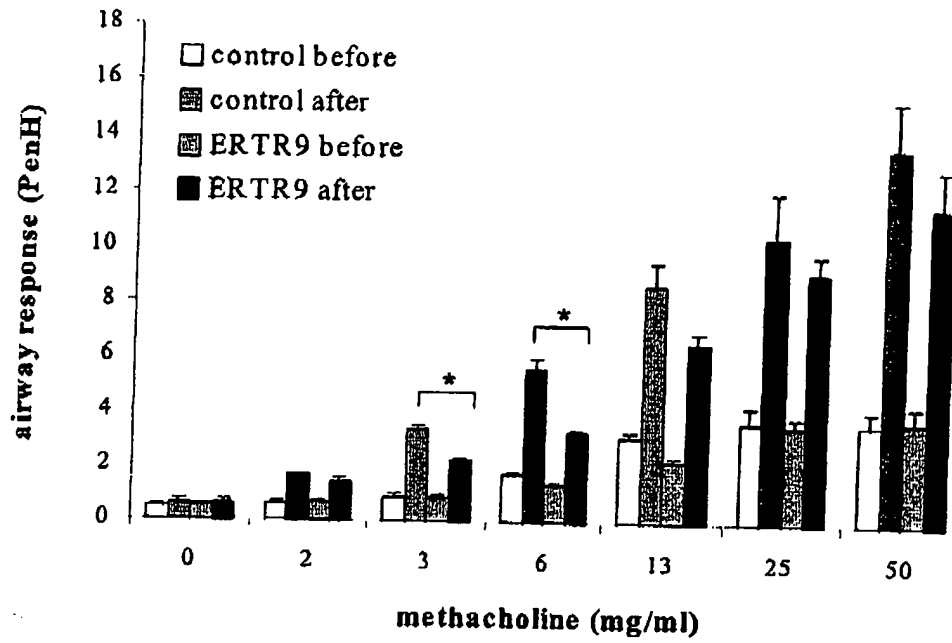
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Fig. 18A



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Fig. 18B



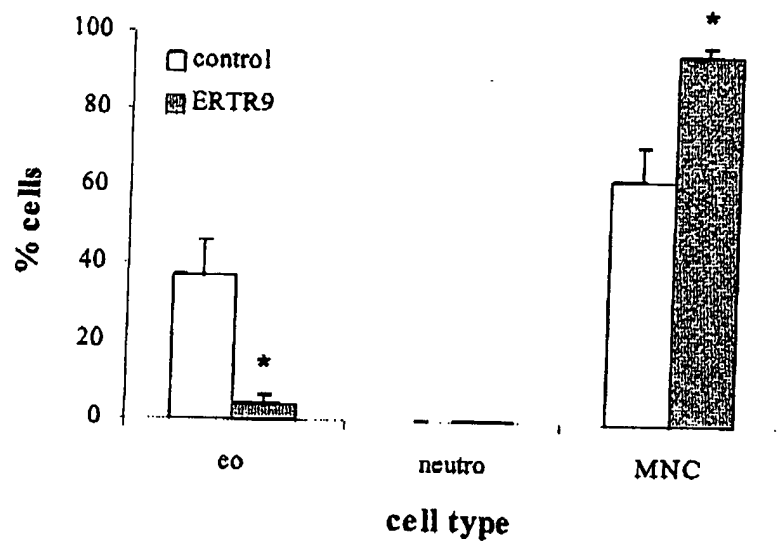
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Fig. 19A



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Fig. 19B

